

570
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OIEP

RAW SEQUENCE LISTING

DATE: 12/05/2001

PATENT APPLICATION: US/09/925,140

TIME: 13:04:59

Input Set : N:\Crf3\RULE60\09925140.txt

Output Set: N:\CRF3\12052001\I925140.raw

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

7 (i) APPLICANT: LAL, PREETI

8 CORLEY, NEIL C.

9 GUEGLER, KARL J.

10 PATTERSON, CHANDRA

12 (ii) TITLE OF INVENTION: SERINE DEHYDRATASE HOMOLOG

14 (iii) NUMBER OF SEQUENCES: 2

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.

18 (B) STREET: 3174 Porter Drive

19 (C) CITY: Palo Alto

20 (D) STATE: CA

21 (E) COUNTRY: USA

22 (F) ZIP: 94304

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Diskette

26 (B) COMPUTER: IBM Compatible

27 (C) OPERATING SYSTEM: Windows

28 (D) SOFTWARE: FastSEQ for Windows Version 2.0b

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/09/925,140

C--> 32 (B) FILING DATE: 08-Aug-2001

33 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: 09/088,435

37 (B) FILING DATE: 1998-06-01

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: Cerrone, Michael C

41 (B) REGISTRATION NUMBER: 39,132

42 (C) REFERENCE/DOCKET NUMBER: PF-0512 US

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: 650-855-0555

46 (B) TELEFAX: 650-845-4166

47 (C) TELEX:

50 (2) INFORMATION FOR SEQ ID NO: 1:

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 325 amino acids

54 (B) TYPE: amino acid

55 (C) STRANDEDNESS: single

56 (D) TOPOLOGY: linear

58 (vii) IMMEDIATE SOURCE:

59 (A) LIBRARY: THP1AZS08

60 (B) CLONE: 2752518

62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

64 Met Asp Gly Pro Val Ala Glu His Ala Lys Gln Glu Pro Phe His Val

65 1

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ENTERED

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66 Val Thr Pro Leu Leu Glu Ser Trp Ala Leu Ser Gln Val Ala Gly Met
67          20          25          30
68 Pro Val Phe Leu Lys Cys Glu Asn Val Gln Pro Ser Gly Ser Phe Lys
69          35          40          45
70 Ile Arg Gly Ile Gly His Phe Cys Gln Glu Met Ala Lys Lys Gly Cys
71          50          55          60
72 Arg His Leu Val Cys Ser Ser Gly Gly Asn Ala Gly Ile Ala Ala Ala
73          65          70          75          80
74 Tyr Ala Ala Arg Lys Leu Gly Ile Pro Ala Thr Ile Val Leu Pro Glu
75          85          90          95
76 Ser Thr Ser Leu Gln Val Val Gln Arg Leu Gln Gly Glu Gly Ala Glu
77          100          105          110
78 Val Gln Leu Thr Gly Lys Val Trp Asp Glu Ala Asn Leu Arg Ala Gln
79          115          120          125
80 Glu Leu Ala Lys Arg Asp Gly Trp Glu Asn Val Pro Pro Phe Asp His
81          130          135          140
82 Pro Leu Ile Trp Lys Gly His Ala Ser Leu Val Gln Glu Leu Lys Ala
83          145          150          155          160
84 Val Leu Arg Thr Pro Pro Gly Ala Leu Val Leu Ala Val Gly Gly Gly
85          165          170          175
86 Gly Leu Leu Ala Gly Val Val Ala Gly Leu Leu Glu Val Gly Trp Gln
87          180          185          190
88 His Val Pro Ile Ile Ala Met His Gly Ala His Cys Phe Asn Ala Ala
89          195          200          205
90 Ile Thr Ala Gly Lys Leu Val Thr Leu Pro Asp Ile Thr Ser Val Ala
91          210          215          220
92 Lys Ser Leu Gly Ala Lys Thr Val Ala Ala Arg Ala Leu Glu Cys Met
93          225          230          235          240
94 Gln Val Cys Lys Ile His Ser Glu Val Val Glu Asp Thr Glu Ala Val
95          245          250          255
96 Ser Ala Val Gln Gln Leu Leu Asp Asp Glu Arg Met Leu Val Glu Pro
97          260          265          270
98 Ala Cys Gly Ala Ala Ala Ile Tyr Ser Gly Leu Leu Arg Arg Leu Gln
99          275          280          285
100 Ala Glu Gly Cys Leu Pro Pro Ser Leu Thr Ser Val Val Val Ile Val
101          290          295          300
102 Cys Gly Gly Asn Asn Ile Asn Ser Arg Glu Leu Gln Ala Leu Lys Thr
103          305          310          315          320
104 His Leu Gly Gln Val
105          325

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107 (2) INFORMATION FOR SEQ ID NO: 2:

108 (i) SEQUENCE CHARACTERISTICS:

109 (A) LENGTH: 1485 base pairs

110 (B) TYPE: nucleic acid

111 (C) STRANDEDNESS: single

112 (D) TOPOLOGY: linear

113 (vii) IMMEDIATE SOURCE:

114 (A) LIBRARY: THPLAZS08

115 (B) CLONE: 2752518

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119      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
121  GGGTCGACCA CCGTCGCATG ATTAGGATGG TGCATGAGTG ATCGGCAGTG CCCGGGAAAG      60
122  CGGTGAGGGT TGCTCTCATC CCTCTCCTC CTCCGTCTTC ACCCGGAGGC TTAGGGTCTG      120
123  GAGCTTTCTC TTAAACAAAG GAGGAGGGAC CAAGGTTGCC GGAAGCTGCC TGAAGCTGGA      180
124  CAGAGCCGGT TCCTGGAAAG AGCTGGTTCC CTGGCAGGCT GGAGGGCAGG AGCTGGGGCC      240
125  ACGCTGGTCT GGGATAGTTG GGCAGGGAGG CTGTCTACCT GGTCTCCAGA ATGGACGGCC      300
126  CTGTGGCAGA GCATGCCAAG CAGGAGCCCT TTCACGTGGT CACACCTCTG TTGGAGAGCT      360
127  GGGCGCTGTC CCAGGTGGCG GGCATGCCTG TCTTCCTCAA GTGTGAGAAT GTGCAGCCCA      420
128  GCGGCTCCTT CAAGATTCCG GCATTGGGGC ATTTCTGCCA GGAGATGGCC AAGAAGGGAT      480
129  GCAGACACCT GGTGTGCTCC TCAGGGGGTA ATGCGGGCAT CGCTGCTGCC TATGCTGCTA      540
130  GGAAGCTGGG CATTCCTGCC ACCATCGTGC TCCCCGAGAG CACCTCCCTG CAGGTGGTGC      600
131  AGAGGCTGCA GGGGGAGGGG GCCGAGGTTT AGCTGACTGG AAAGGTCTGG GACGAGGCCA      660
132  ATCTGAGGGC GCAAGAGTTG GCCAAGAGGG ACGGCTGGGA GAATGTCCCC CCGTTTGACC      720
133  ACCCCCTAAT ATGGAAGAGC CACGCCAGCC TGGTGAGGA GCTGAAAGCA GTGCTGAGGA      780
134  CCCACACAGG TGCCCTGGTG CTGGCAGTTG GGGGTGGGGG TCTCCTGGCC GGGGTGGTGG      840
135  CTGGCCTGCT GGAGGTGGGC TGGCAGCATG TACCCATCAT TGCCATGGAG ACCCATGGGG      900
136  CAACTGCTT CAATGCGGCC ATCACAGCCG GCAAGCTGGT CAACTTCCA GACATACCA      960
137  GTGTGGCCAA GAGCCTGGGT GCCAAGACGG TGGCCGCTCG GGCCCTGGAG TGCATGCAGG      1020
138  TGTGCAAGAT TCACTCTGAA GTGGTGGAGG ACACCGAGGC TGTGAGCGCT GTGCAGCAGC      1080
139  TCCTGGATGA TGAGCGTATG CTGGTGGAGC CTGCCTGTGG GGCAGCCTTA GCAGCCATCT      1140
140  ACTCAGGCCCT CCTGCGGAGG CTCCAGGCCG AGGGCTGCCT GCCCCCTTCC CTGACTTCAG      1200
141  TTGTGGTAAT CGTGTGTGGA GGCAACAACA TCAACAGCCG AGAGCTGCAG GCTTTGAAAA      1260
142  CCCACCTGGG CCAGGTCTGA GGGGTCCCAT CCTGGCCCCA AAGACCCCTG AGAGGCCCCAT      1320
143  GGACAGTCCT GTGTCTGGAT GAGGAGGACT CAGTGCTGGC AGATGGCAGT GGAAGCTGCC      1380
144  CTGTGCAACT GTGCTGGCTG CCTCCTGAAG GAAGCCCTCC TGGACTGCTT CTTTGGGCTC      1440
145  TCCGACAACT CCGGCCAATA AACACTTTCT GAATTGAAAA AAAAA      1485

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VERIFICATION SUMMARY

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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]